

1/8

10 30 50
AAAGCACAGACTTCAGGTCTCCAAGGAGGATGGGTGGCTGCAGCACAAGAGGCAAGCGGC
M G G C S T R G K R P

70 90 110
CGTCAGCCCTCAGTCTGCTGCTGCTGCTGCTGCTCGGGGATCGCAGCCTCTGCCCTCC
S A L S L L L L L L L S G I A A S A L P
↑

130 150 170
CCCTGGAGAGCGGTCCCACCGGCCAGGACAGTGTGCAGGATGCCACAGGCGGGAGGAGGA
L E S G P T G Q D S V Q D A T G G R R T

190 210 230
CCGGCCTTCTGACTTTTCCTTGCTGGTGGCATGAGTGGGCTTCCCAAGACAGCTCCAGCA
G L L T F L A W W H E W A S Q D S S S T

250 270 290
CCGCTTTTGAAGGGGTACCCCGGAGCTGTCTAAGCGGCAGGAAAGACCACCCCTCCAGC
A F E G G T P E L S K R Q E R P P L Q Q

310 330 350
AGCCCCACACCGGGATAAAAAGCCCTGCAAGAACTTCTTCTGGAAAACCTTCTCCTCGT
P P H R D K K P C K N F F W K T F S S C

370 390 410
GCAAGTAGCCCGAGCCTGACCGGAGCCTGACCGGCCACCCTGTGAATGCAGCCGTGGCCT
K

430
GAATAAAGAGTGTCAAGT

FIGURE 1

CST 10 RPSALSLLLLLLLLSGIAASALPLESGPTGQDSVQDATGGRRTGLLTFLAW 59
SST 7 QCALAALCIVLAGGVGTGAPSDPRLRQFLQKSLAAATGKQELAKYFLAEL 56

CST 60 WHEWASQDSSSTAFEGGTPELSKQERPPLOQ.....PPHRDKKPK 101
SST 57 LSEPNQTENDALEPEDLPQAAEQDEMRLLELQRSANSNPAMAPREKAGCK 106

CST 102 NFEWKTFTSSCK
SST 107 NFEWKTFTTSC

FIGURE 2

| | |
|---|-----|
| GCACGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA GGA GGC | 51 |
| Met Met Gly Gly Arg Gly Thr Gly Gly | |
| 1 5 | |
| AAG TGG CCC TCA GCC TTC GGG <u>CTG CTG CTG</u> CTC TGG GGG GTC GCA GCC | 99 |
| Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Leu Trp Gly Val Ala Ala | |
| 10 15 20 25 | |
| TCC GCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG | 147 |
| Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln | |
| 30 35 40 | |
| GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GCC TGG TGG | 195 |
| Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp | |
| 45 50 55 | |
| CAC GAG TCG GCT TCC CAA GCC AGC TCC AGC ACC CCC GTC GGA GGG GGT | 243 |
| His Glu Trp Ala Ser Gln Ala Ser Ser Ser Thr Pro Val Gly Gly Gly | |
| 60 65 70 | |
| ACC CCC GGG CTG TCC AAG AGC <u>CAG GAA AGG CCA CCC CCC CAA CAG CCC</u> | 291 |
| Thr Pro Gly Leu Ser Lys Ser <u>Gln Glu Arg Pro Pro Pro Gln Gln Pro</u> | |
| 75 80 85 | |
| CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC | 339 |
| <u>Pro His Leu Asp</u> Lys Lys <u>Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe</u> | |
| 90 95 100 105 | |
| TCC TCG TGC AAG TAA CCC CAC CCT GGG CAT AGC ACC CTG GCC ACC CTG | 387 |
| <u>Ser Ser Cys Lys</u> * | |
| 110 115 120 | |
| TGA GAT GCC AAC GAG ACC TGA ATA AAG ACT GTC AAT CAA C | 427 |
| 125 130 | |

FIGURE 3

| | | | | | |
|-----------|-------------------|-------------------|-------------------|-------------|------------|
| MOUSE CST | | ...GCACGAG | GCTCAGCAGG | TCCGAGGATG | ATGGGTGGCC |
| RAT CT | | .AAAGCACAG | ACTTCAGGTC | TCCAAGGAGG | ATGGGTGGCT |
| HUMAN CST | GGCACGAGGC | CAAACATTGA | TTTCAGGGCT | GCCAGGAGG | AAGAGCAGCA |
| | | | | | |
| MOUSE CST | GAGGCACAGG | AGGCAAGTGG | CCCTCAG... | |CCTTC |
| RAT CST | GCAGCACAAG | AGGCAAGCGG | CCGTCAG... | |CCCTC |
| HUMAN CST | GCAGGGTGGG | AGAGAAGCTC | CAGTCAGCCC | ACAAGAAGCC | ATTGTCCCC |
| | | | | | |
| MOUSE CST | GG..... | <u>.GCTGCTGCT</u> | <u>GCTCTGGGGG</u> | GTGCGAGCCT | CCGCCCTTCC |
| RAT CST | <u>AGTCTGCTGC</u> | <u>TGCTGCTGCT</u> | <u>GCTCTCGGGG</u> | ATCGCAGCCT | CTGCCCTCCC |
| HUMAN CST | <u>GGCCTCCTGC</u> | <u>TGCTGCTGCT</u> | CTCCGGGGCC | ACGGCCACCG | CTGCCCTGCC |
| | | | | | |
| MOUSE CST | CCTGGAGAGT | GGCCCTACTG | GCCAGGACAG |TGTG | CAGGAAGCCA |
| RAT CST | CCTGGAGAGC | GGTCCCACCG | GCCAGGACAG |TGTG | CAGGATGCCA |
| HUMAN CST | CCTGGAGGGT | GGCCCCACCG | GCCGAGACAG | CGAGCATATG | CAGGAAGCGG |
| | | | | | |
| MOUSE CST | C...CGAGGG | GAGGAGCGGC | CTTCTGACTT | TCCTTGCCCTG | GTGGCAGCAG |
| RAT CST | CAGGCGGGAG | GAGGACCGGC | CTTCTGACTT | TCCTTGCCCTG | GTGGCATGAG |
| HUMAN CST | CAGGAATAAG | GAAAAGCAGC | CTCCTGACTT | TCCTCGCTTG | GTGGTTTGAG |
| | | | | | |
| MOUSE CST | TGGGCTTCCC | AAGCCAGCTC | CAGCACCCCC | GTGGGAGGGG | GTACCCCCGG |
| RAT CST | TGGGCTTCCC | AAGACAGCTC | CAGCACCGCT | TTCGAGGGG | GTACCCCCGA |
| HUMAN CST | TGGACCTCCC | AGGCCAGTGC | CGGGCCCCCTC | ATAGGAGAGG | AAGCCCCGGA |
| | | | | | |
| MOUSE CST | GCTGTCCAAG | AGCCAGGAAA | GGCCACCCCC | CCAACAGCCC | CCACACCTGG |
| RAT CST | GCTGTCTAAG | CGGCAGGAAA | GACCACCCCT | CCAGCAGCCC | CCACACCGGG |
| HUMAN CST | GGTGGCCAGG | CGGCAGGAAG | GCGCACCCCC | CCAGCATATC | GCGCGCCGGG |
| | | | | | |
| MOUSE CST | ATAAAAAGCC | CTGCAAGAAC | TTCTTCTGGA | AAACCTTCTC | CTCGTGCAAG |
| RAT CST | ATAAAAAGCC | CTGCAAGAAC | TTCTTCTGGA | AAACCTTCTC | CTCGTGCAAG |
| HUMAN CST | ACAGAATGCC | CTGCAGGAAC | TTCTTCTGGA | AGACCTTCTC | CTCCTGCAAA |
| | | | | | |
| MOUSE CST | TAACCCACC | CTGGGCATAG | CACCCTGGCC | ACCCTGTGAG | ATGCCAACGA |
| RAT CST | TAGCCCGAGC | CTGACCGGAG | CCTGACCGGC | CACCCTGTGA | ATGCAGCCGT |
| HUMAN CST | TAAAACCTCA | CCCATGAATG | C..... | .TCACGCAAG | TGTAATGACA |
| | | | | | |
| MOUSE CST | GACCTGAATA | AAGACTGTCA | ATCAAC.... | | |
| RAT CST | GGCCTGAATA | AAGAGTGTCA | AGT..... | | |
| HUMAN CST | GACCTGAATA | AAATGTATTA | AGCAGCAGTG | ATCTTTCTCT | TCCTCCTTCC |
| | | * | | | |
| | | | | | |
| MOUSE CST | | | | | |
| RAT CST | | | | | |
| HUMAN CST | CAAGTCATTG | AAAAGTGTTT | GTTATTTAAA | TTCCAATAAT | GCCCAATACT |
| | | | | | |
| MOUSE CST | | | | | |
| RAT CST | | | | | |
| HUMAN CST | GACGTGTCTT | GAGTAATTTG | GAACCCAAAA | GTGAAGATCT | TTGATAAAGA |
| | | | | | |
| MOUSE CST | | | | | |
| RAT CST | | | | | |
| HUMAN CST | TTTTTTTTGT | GGTTCGACTG | GACTGTGCTG | AGTGC3GGCA | CTGGGCTTTT |
| | | | | | |
| MOUSE CST | | | | | |
| RAT CST | | | | | |
| HUMAN CST | CTTCTGATGT | TCATTATGGT | GCTGGGAAGC | TCTGTCTTTG | ATTTAAATA |
| | | | | | * |
| | | | | | |
| MOUSE CST | | | | | |
| RAT CST | | | | | |
| HUMAN CST | AAATAGCTAA | AGGCTACAC | | | |

FIGURE 3a

| | | | | | |
|-----------|------------|------------|------------|------------|------------|
| | 1 | | | | 50 |
| RAT CST | .MGGCSTRGK | RPSALSLLLL | LLLSGIAASA | LPLESGPTGQ | DS..VQDATG |
| MOUSE CST | MMGGRGTGGK | WPSAFGLLLL | W...GVAASA | LPLESGPTGQ | DS..VQEATE |
| HUMAN CST | | MPLSPGLLLL | LLSGATATAA | LPLEGGPTGR | DSEHMQEAAG |
| Consensus | ----- | -P---LLLL | -----A--A | LPLE-GPTG- | DS---Q-A-- |

| | | | | | |
|-----------|------------|------------|------------|--------------------------|-------------|
| | 51 | | | | 100 |
| RAT CST | GRRTGLLTFL | AWWHEWASQD | SSSTAFEGGT | P ELSK RQERP | PLQQPPHRDK |
| MOUSE CST | G.RSGLLTFL | AWWHEWASQA | SSSTPVGGGT | PGLSKSQERP | PPQQPPHLDK |
| HUMAN CST | IRKSSLLTFL | AWWFEWTSQA | SAGPLIGEEA | REVAR RRQ EGA | PPQQSARRDR |
| Consensus | -----LLTFL | AWW-EW-SQ- | S----- | -----QE-- | P-QQ-----D- |

| | | | |
|-----------|------------|-------|-----|
| | 101 | | 116 |
| RAT CST | KPCKNFFWKT | FSSCK | |
| MOUSE CST | KPCKNFFWKT | FSSCK | |
| HUMAN CST | MPCRNFFWKT | FSSCK | |
| Consensus | -PC-NFFWKT | FSSCK | |

FIGURE 3b

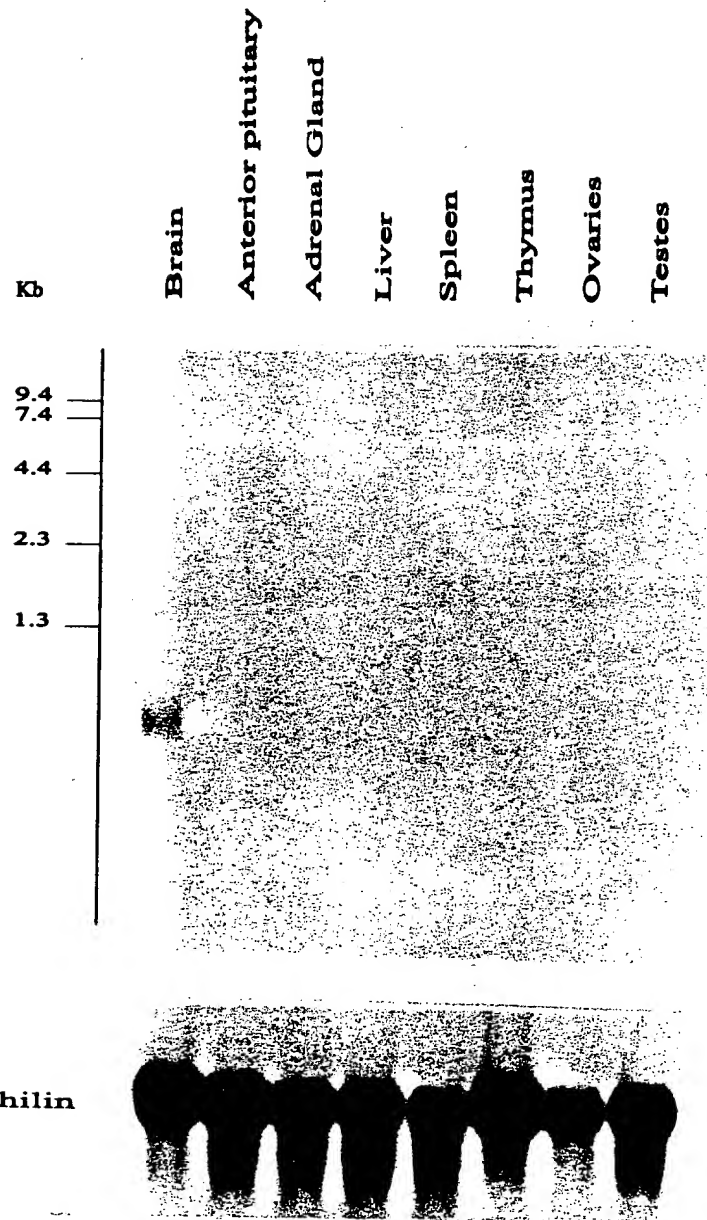
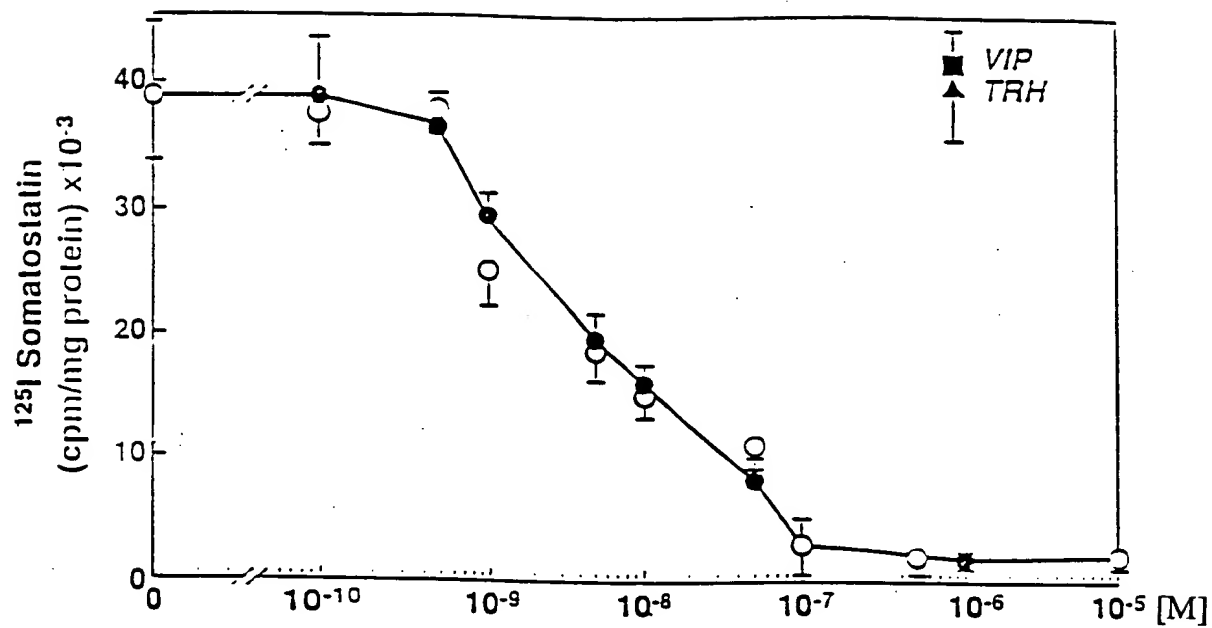
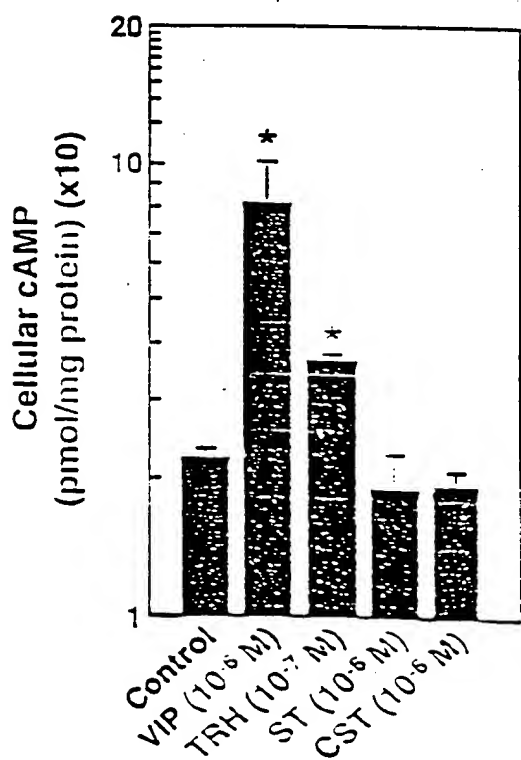


FIGURE 4

5A



5B



5C

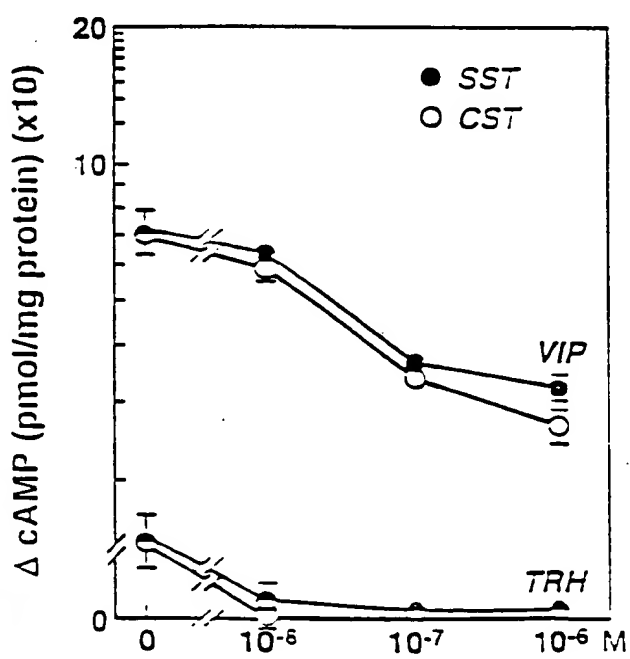
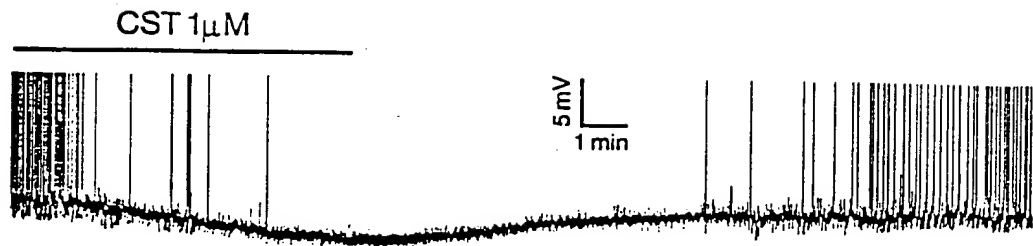
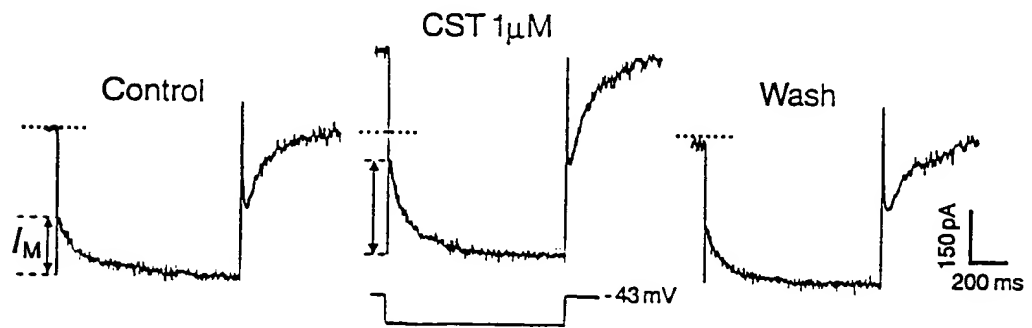


FIGURE 5

6A



6B



6C

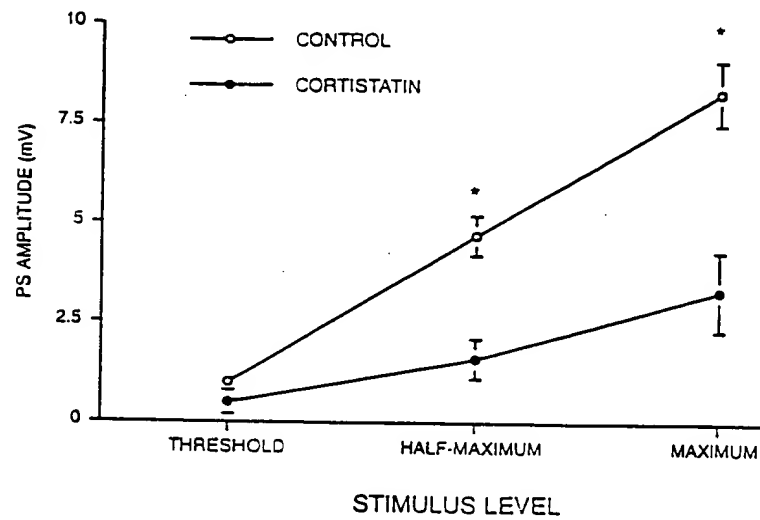
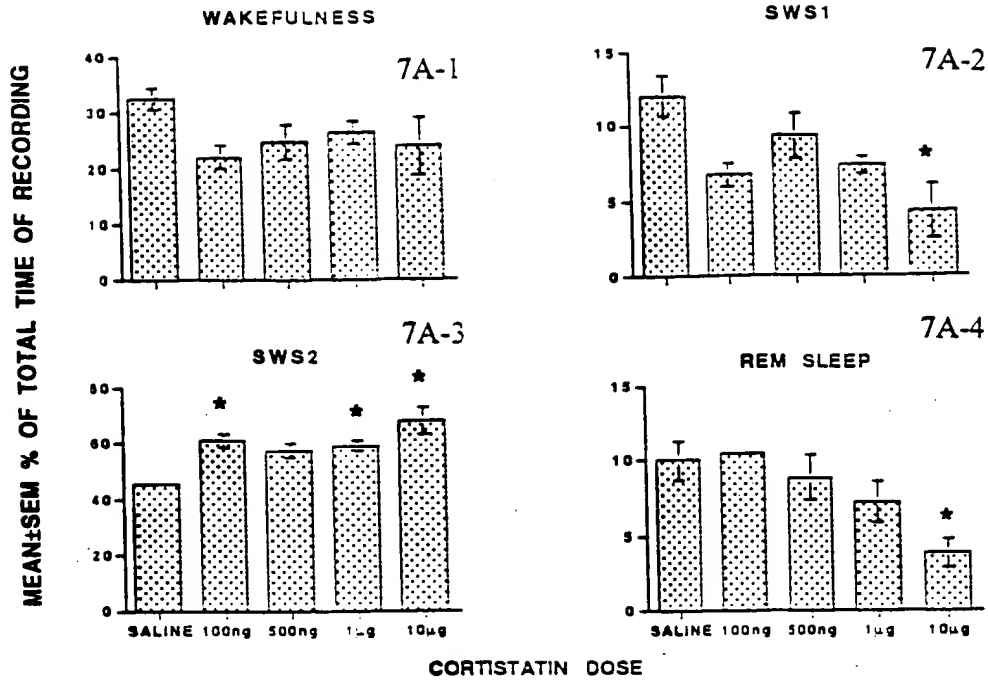
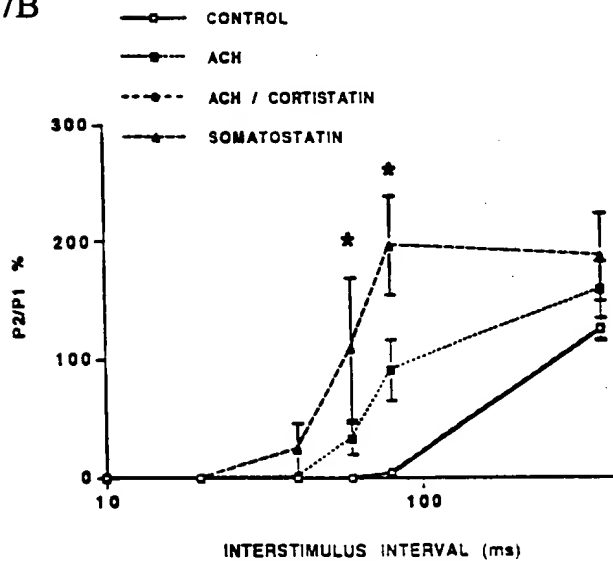


FIGURE 6

7A



7B



7C

7D

7E

7F

7G

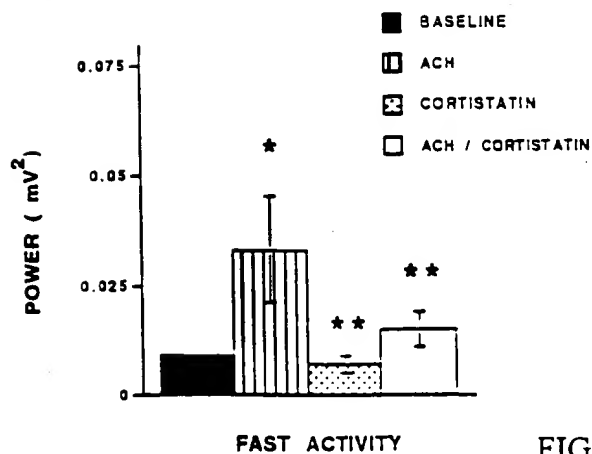


FIGURE 7